

# Efficient Numerical Methods for the Solution and Parameter Estimation in Multiscale Models of Hepatitis C Viral Kinetics

Wednesday September 22nd at 1:00 pm

Location: CULM 611

Zoom Link: <https://us02web.zoom.us/j/87468079122?pwd=VDRkeUhVOUU1cmt0RWErSnRNVTKrUT09>

Age-structured multiscale models have been developed to study viral kinetics. However, they are notoriously difficult to solve and when utilizing this type of models parameter estimation presents a challenge. Here, we investigate the numerical solutions of a multiscale model of hepatitis C virus (HCV) dynamics during antiviral treatment and compare them with analytical approximations. First, we show that considerable gain in efficiency can be achieved by using adaptive stepsize methods over fixed stepsize methods for simulating realistic scenarios when solving multiscale models numerically. We compare between several numerical schemes that are suitable and show the benefit of using the Rosenbrock method, an implicit adaptive stepsize method that is both efficient and stable. Second, we address parameter estimation by constrained optimization and show that derivative-free methods such as Powell's constrained optimization by linear approximation (COBYLA) provides an efficient procedure for this task. For simulating trajectories of viral hepatitis progression or decline in patients who are treated with antiviral drugs, we developed a simulator with a graphical user interface. Machine learning of data from patients is now being incorporated.

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